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| 09/888,224 | 06/22/2001 | Jay M. Short | DIVER1150-6 | 8097 |

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GRAY CARY WARE & FREIDENRICH LLP
4365 EXECUTIVE DRIVE
SUITE 1100
SAN DIEGO, CA 92121-2133

| EXAMINER | |
|---|---|
| WHISENANT, ETHAN C | |

| ART UNIT | PAPER NUMBER |
|---|---|
| 1634 | |

DATE MAILED: 11/03/2003

Please find below and/or attached an Office communication concerning this application or proceeding.

| Office Action Summary | Applicati n No. | Applicant(s) | |
|---|---|---|---|
| | 09/888,224 | SHORT ET AL. | |
| | Examin r | Art Unit | |
| | Ethan Whisenant, Ph.D. | 1634 | |

*-- The MAILING DATE of this communication appears on the cover sheet with the correspondence ddress --*

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

1)☒ Responsive to communication(s) filed on *23 July 2003* .

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

4)☒ Claim(s) *42-55 and 88-114* is/are pending in the application.

4a) Of the above claim(s) *113 and 114* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *42-55, 88-104 and 110-112* is/are rejected.

7)☒ Claim(s) *105-109* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

**Application Papers**

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

**Priority under 35 U.S.C. §§ 119 and 120**

13)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

**Attachment(s)**

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____ .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

## FINAL REJECTION

**1.** The applicant's Response (filed 23 JUL 03) to the Office Action has been entered. Following the entry of the claim amendment(s), **Claim(s) 42-55 and 88-114** is/are pending with Claims 113-114 withdrawn as they are drawn to a non elected invention (i.e. **Group I** and/or **Group II** of the restriction requirement mailed 23 AUG 02). Rejections and/or objections not reiterated from the previous office action are hereby withdrawn. The following rejections and/or objections are either newly applied or reiterated. They constitute the complete set presently being applied to the instant application. An action on **Claim(s) 42-55 and 88-112** follows.

### 35 USC § 112- 2ND PARAGRAPH

**2.** The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

### CLAIM REJECTIONS under 35 USC § 112- 2ND PARAGRAPH

**3.** **Claim(s) 89-92 and 111-112** is/are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

**Claim 89** is vague and indefinite because the phrase "the library which exhibits a desired activity" lacks proper antecedent basis in Claim 88.

**Claim 111** is vague and indefinite because the phrase "identifying a modified nucleic acid having an endoglucanase activity" lacks proper antecedent basis and it makes the claim confusing. Beyond riobozymes, nucleic acids lack enzymatic activity. **Please clarify.** Furthermore, the examiner cannot find basis in the specification for a nucleic acid having an endoglucanase activity. Please note that for the evaluation of this claim against the prior art the examiner has assumed that this claim reads as follows:

**Claim 111 (as best interpreted by the examiner)** A method of generating and identifying a nucleic acid encoding an endoglucanse comprising:

obtaining a nucleic acid encoding an endoglucanase comprising a sequence having at least about 50 % identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto;

modifying one or more nucleotides in said sequence to another nucleotide deleting one or more nucleotides in the sequence or adding one or more nucleotides to said sequence;

identifying a modified nucleic acid encoding a polypeptide having an endoglucanase activity.

**Claim 112** is vague and indefinite because the phrase "wherein the polypeptide has at least 50% sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto" lacks proper antecedent basis because SEQ ID NO: 1 is a nucleic acid sequence not a polypeptide sequence. **Please clarify.** Please note that for the evaluation of this claim against the prior art the examiner has assumed that this claim reads as follows:

**Claim 112 (as best interpreted by the examiner)** A method for modifying small molecules such that the small molecule has a desired activity comprising:

providing a polypeptide having an endoglucanase activity and encoded by a polynucleotide comprising a sequence having at least about 50 % identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto;

providing a small molecule;

mixing the polypeptide with the small molecule to produce a modified small molecule;

testing the modified small molecule for the desired activity.

## 35 USC § 102

**4.** The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that may form the basis for rejections set forth in this Office action:

> A person shall be entitled to a patent unless --
>
> **(a)** the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> **(b)** the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
>
> ***(e)*** The invention was described in –
> (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effect under this subsection of a national application published under section 122(b) only if the international application designating the United States was published under Article 21(2)(a) of such treaty in the English language; or
> (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that a patent shall not be deemed filed in the United States for the purposes of this subsection based on the filing of an international application filed under the treaty defined in section 351(a)

## CLAIM REJECTIONS UNDER 35 USC § 102

**5.** **Claim(s) 88, 95-98, 110 and 112** is/are rejected under 35 U.S.C. 102(b) as being anticipated by Knowles et al. [US 5,393,670 (1995)].

**Claim 88** is drawn to a method for modifying small molecules comprising three required steps. To begin, a polypeptide encoded by a polynucleotide comprising a sequence having at least about 50 % identity to SEQ ID NO: 1 and having an endoglucanase activity is provided. Next, a small molecule is provided and finally, the polypeptide is mixed with the small molecule to produce a modified small molecule.

**Claim 96** is drawn to a method for modifying small molecules comprising three required steps. To begin, a polypeptide having an endoglucanase activity and encoded by a polynucleotide comprising a sequence as set forth SEQ ID NO: 1 is provided. Next, a small molecule is provided and finally, the polypeptide is mixed with the small molecule to produce a modified small molecule.

Knowles et al. teach a method for modifying small molecules comprising the three steps recited in Claims 88 and 96. See for example Column 9, beginning at about line 42. The polypeptide provided is the EGI found secreted in the growth medium and expressed out of VTT-RC-84013 (i.e. a polynucleotide comprising a sequence having at least about 50 % identity to SEQ ID NO: 1. **Please note that th phrase "comprising a sequenc " on line 3 of Claims 88 and 96 can be interpreted to mean two**

**nucleotides all the way up to the full length nucleic acid sequence (i.e. SEQ ID NO: 1).** The small molecule provide is β-glucan while the modified small molecule is the hydrolysis product of β-glucan (i.e. glucose).

**Claim 95** is drawn to a method for modifying small molecules comprising three required steps. To begin, a polypeptide having an endoglucanase activity wherein the polypeptide is encoded by a nucleic acid comprising at least 30 consecutive residues of a sequence having at least about 50% sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto, is provided. Next, a small molecule is provided and, finally, the polypeptide is mixed with the small molecule to produce a modified small molecule.

Knowles et al. teach a method for modifying small molecules comprising the three steps recited in Claim 95. See for example Column 9, beginning at about line 42. The polypeptide provided is the EGI found secreted in the growth medium and expressed out of VTT-RC-84013 (i.e. a nucleic acid comprising at least 30 consecutive residues of a sequence having at least about 50% sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto **Note the alignment provided by the applicant and see at least nucleotide positions 2280-2309 of applicant's SEQ ID NO: 1. Note that the sequence of Knowles et al. (i.e. the sequence in the top row) comprises a sequence of least 30 consecutive residues which has 18/30 (60%) identical nucleotides (i.e. it has at least about 50% sequence identity to a sequence of at least 30 consecutive residues as set forth in SEQ ID NO: 1").** The small molecule provided is β-glucan while the modified small molecule produced is the hydrolysis product of β-glucan (i.e. glucose).

**Claim 97** is drawn to an embodiment of Claim 93 or **95** wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 55% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 95 above.

**Claim 98** is drawn to an embodiment of Claim 97 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 60% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 95 above.

**Claim 110** is drawn to an embodiment of the method of Claim 93 or **95** wherein the endoglucanase activity comprises a carboxymethyl cellulase activity. Admittedly, Knowles et al. do not explicitly teach that their recombinant enzyme(s) (i.e. their endoglucanase(s) comprise a carboxymethyl

cellulase activity. However, absent a showing to the contrary, its is believed that this limitation is inherent to the endoglucanase(s) taught by Knowles et al.

**Claim 112** is drawn to a method for modifying small molecules such that the small molecule has a desired activity which method comprises three required steps: to begin a polypeptide having an endoglucanase activity and encoded by a polynucleotide comprising a sequence having at least about 50 % identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto is provided. Next, a small molecule is provided. Then, the polypeptide is mixed with the small molecule to produce a modified small molecule. Finally, the modified small molecule is tested for a desired activity.

Knowles et al. teach a method for modifying small molecules comprising the steps recited in Claim 112. See for example Column 9, beginning at about line 42. The polypeptide provided is the EGI found secreted in the growth medium and expressed out of VTT-RC-84013 (i.e. a nucleic acid comprising a sequence having at least about 50% sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto. **Note the alignment provided by the applicant and see at least nucleotide positions 2280-2309 of applicant's SEQ ID NO: 1. Note that the sequenc of Knowles et al. (i.e. the sequence in the top row) comprises a sequence of least 30 consecutive residues which has 18/30 (60%) identical nucleotides (i.e. it has at least about 50% sequence identity to a sequence of at least 30 consecutive residues as set forth in SEQ ID NO: 1").** The small molecule provided is β-glucan while the modified small molecule produced is the hydrolysis product of β-glucan (i.e. glucose). The modified small molecule tested for a desired activity is the glucose using the dinitro salisylic acid method.

**6.** **Claim(s) 88, 95-104 and 110** is/are rejected under 35 U.S.C. 102(e) as being anticipated by Thomas et al. [US 5,536,65 (1996)].

**Claim 88** is drawn to a method for modifying small molecules comprising three required steps. To begin, a polypeptide encoded by a polynucleotide comprising a sequence having at least about 50% identity to SEQ ID NO: 1 and having an endoglucanase activity is provided. Next, a small molecule is provided and finally, the polypeptide is mixed with the small molecule to produce a modified small molecule.

**Claim 96** is drawn to a method for modifying small molecules comprising three required steps. To begin, a polypeptide having an endoglucanase activity and encoded by a polynucleotide

comprising a sequence as set forth SEQ ID NO: 1 is provided. Next, a small molecule is provided and finally, the polypeptide is mixed with the small molecule to produce a modified small molecule.

Thomas et al. teach a method for modifying small molecules comprising the three steps recited in Claims 88 and 96. See for example the abstract. The polypeptide provided is the modified EGI endoglucanase enzyme which has a sequence having at least about 50% identity to SEQ ID NO: 1. **Note the alignment provided by the examiner in attached Appendix A. Note nucleotides 1925-1954 of SEQ ID NO:6 of Thomas et al. as compared to nucleotides 1006-1035 of SEQ ID NO: 1 of the instant application. Note that the sequence of Thomas et al. (i.e. the sequence in the top row) comprises a sequence of least 30 consecutive residues which has 27/30 (90%) identical nucleotides (i.e. it has at least about 50% sequence identity to a sequence of at least 30 consecutive residues as set forth in SEQ ID NO: 1"). Also, as regards the language of Claims 88 and 96, please note that the phrase "comprising a sequence" on line 3 can be interpreted to mean two nucleotides all the way up to the full length nucleic acid sequence (i.e. SEQ ID NO: 1).** The small molecule provided is cellulose while the modified small molecule is the hydrolysis product of the cellulose (i.e. the sugars).

**Claim 95** is drawn to a method for modifying small molecules comprising three required steps. To begin, a polypeptide having an endoglucanase activity wherein the polypeptide is encoded by a nucleic acid comprising at least 30 consecutive residues of a sequence having at least about 50% sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto, is provided. Next, a small molecule is provided and finally, the polypeptide is mixed with the small molecule to produce a modified small molecule.

Thomas et al. teach a method for modifying small molecules comprising the three steps recited in Claim 95. See, for example, the abstract. The polypeptide provided is the modified EGI endoglucanase enzyme which has a sequence having at least about 50% identity to SEQ ID NO: 1. **Note the alignm nt provided by the examiner in attached Appendix A. Note nucleotides 1925-1954 of SEQ ID NO:6 of Thomas et al. as compared to nucleotides 1006-1035 of SEQ ID NO: 1 of the instant application. Note that the sequence of Thomas et al. (i.e. the sequence in the top row) comprises a sequence of least 30 consecutive residues which has 27/30 (90%) identical nucleotides (i.e. it has at least about 50% sequence identity to a sequence of at least 30 consecutive residues as set forth in SEQ ID NO: 1").** The small molecule provided is cellulose while the modified small molecule is the hydrolysis product of the cellulose (i.e. the sugars).

**Claim 97** is drawn to an embodiment of Claim 93 or **95** wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 55% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 95 above.

**Claim 98** is drawn to an embodiment of Claim 97 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 60% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 95 above.

**Claim 99** is drawn to an embodiment of Claim 98 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 65% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 95 above.

**Claim 100** is drawn to an embodiment of Claim 99 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 70% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 95 above.

**Claim 101** is drawn to an embodiment of Claim 100 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 75% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 95 above.

**Claim 102** is drawn to an embodiment of Claim 101 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 80% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 95 above.

**Claim 103** is drawn to an embodiment of Claim 102 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 85% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 95 above.

**Claim 104** is drawn to an embodiment of Claim 103 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 90% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 95 above.

**Claim 110** is drawn to an embodiment of the method of Claim 93 or **95** wherein the endoglucanase activity comprises a carboxymethyl cellulase activity.

Admittedly, Thomas et al. do not explicitly teach that their recombinant enzyme(s) (i.e. their endoglucanase(s) comprise a carboxymethyl cellulase activity. However, absent a showing to the contrary, its is believed that this limitation is inherent to the endoglucanase(s) taught by Thomas et al.

**35 USC § 103**

**7.** The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> **(a)** A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

**8.** This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. § 103, the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligations under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of potential 35 U.S.C. § 102(f) or (g) prior art under 35 U.S.C. § 103.

**CLAIM REJECTIONS UNDER 35 USC § 103**

**9.** **Claim(s) 42-55, 93-94, 97-98, and 110-111** is/are rejected under 35 U.S.C. 103(a) as being unpatentable over Stemmer [US 6,277,638 (2001)] in view of Knowles et al. [US 5,393,670 (1995)].

**Claim 42** is drawn to a method of generating a variant which comprises two required steps. To begin, a nucleic acid encoding an endoglucanase comprising a sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto is obtained. Next one or more nucleotides in said sequence are modified to another nucleotide or one or more nucleotides in said sequence are deleted or one or more nucleotides are added to said sequence.

Stemmer teaches a method of mutagenesis which comprises all of the limitations set forth in Claim 42 except these authors do not teach a nucleic acid as recited in Claim 42. However, Knowles et al. do teach a recombinant DNA vector encoding an endoglucanase (i.e. EGI) and comprising a nucleic acid sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1. **Note that the phrase "comprising a sequence" in Claims 42 has been interpreted broadly to mean two nucleotides. The phrasing used (i.e. "comprising a sequence") can be interpreted to mean two nucleotides all the way up to the full length nucleic acid sequence (i.e. SEQ ID NO: 1). Also, note the alignment provided by the applicant and see at least nucleotide positions 2280-2309 of applicant's SEQ ID NO: 1 and note that the sequence of Knowles et al. (i.e. the sequence in the top row) comprises a sequence of least 30 consecutive residues which has 18/30 (60%) identical nucleotides (i. . has at least about 50% sequence identity) to a sequence as set forth in SEQ ID NO: 1".**

In addition, Stemmer teaches using his method (i.e. recursive DNA shuffling by fragmentation, reassembly and selection) to improve and/or optimize the yield, stability, and/or enzymatic capability of

proteins. Therefore, absent an unexpected result it would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention to modify the method of Stemmer wherein a recombinant DNA vector encoding an endoglucanase and comprising a sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto as taught by Knowles et al. was mutagenized. The motivation for making the modification recited above would have been to improve and/or optimize the yield, stability, and/or enzymatic capability of the endoglucanase taught by Knowles et al. Also, absent an unexpected result, the substitution of one well known reagent with known properties for a second well known reagent with known properties is routine in the art. As regards the motivation to make the substitution recited above, the motivation to combine arises from the expectation that the prior art elements will perform their expected functions to achieve their expected results when combined for their common known purpose. Support for making this obviousness rejection comes from the M.P.E.P. at 2144.07 and 2144.09.

**Claim 93** is drawn to a method of generating a nucleic acid encoding an endoglucanase which method comprises two required steps. To begin, a nucleic acid encoding an endoglucanase, wherein the nucleic acid comprises at least 30 consecutive residue of a sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto is obtained. Next one or more nucleotides in said sequence are modified to another nucleotide deleting one or more nucleotides in the sequence or adding one or more nucleotides in the sequence are added to said sequence.

Stemmer teaches a method of mutagenesis which comprises all of the limitations set forth in Claim 93 except these authors do not teach a nucleic acid as recited in Claim 93. However, Knowles et al. do teach a recombinant DNA vector encoding an endoglucanase (i.e. EGI) and "comprising at least 30 consecutive residue of a sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1". **Note the alignment provided by the applicant and see at least nucleotide positions 2280-2309 of applicant's SEQ ID NO: 1 and note that the sequence of Knowles et al. (i.e. the sequence in the top row) comprises a sequence of least 30 consecutive residues which has 18/30 (60%) identical nucleotides (i.e. has at least about 50% sequence identity) to a sequence as set forth in SEQ ID NO: 1".**

In addition, Stemmer teaches using his method (i.e. recursive DNA shuffling by fragmentation, reassembly and selection) to improve and/or optimize the yield, stability, and/or enzymatic capability of proteins. Therefore, absent an unexpected result it would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention to modify the method of Stemmer wherein a recombinant DNA vector encoding an endoglucanase and comprising a sequence having at least about

50 % sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto as taught by Knowles et al. was mutagenized. The motivation for making the modification recited above would have been to improve and/or optimize the yield, stability, and/or enzymatic capability of the endoglucanase taught by Knowles et al. Also, absent an unexpected result, the substitution of one well known reagent with known properties for a second well known reagent with known properties is routine in the art. As regards the motivation to make the substitution recited above, the motivation to combine arises from the expectation that the prior art elements will perform their expected functions to achieve their expected results when combined for their common known purpose. Support for making this obviousness rejection comes from the M.P.E.P. at 2144.07 and 2144.09.

**Claim 94** is drawn to a method of generating a nucleic acid encoding an endoglucanase which method comprises two required steps. To begin, a nucleic acid comprising a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto is obtained. Next one or more nucleotides in said sequence are modified to another nucleotide, deleting one or more nucleotides in the sequence or adding one or more nucleotides in the sequence are added to said sequence.

Stemmer teaches a method of mutagenesis which comprises all of the limitations set forth in Claim 94 except these authors do not teach a nucleic acid as recited in Claim 94. However, Knowles et al. do teach a recombinant DNA vector encoding an endoglucanase (i.e. EGI) and comprising a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto. **Note that the phrase "comprising a sequence" in Claims 94 has been interpreted broadly to mean two nucleotides. The phrasing used (i.e. "comprising a sequence") can be reasonably be interpreted to mean - two nucleotides all the way up to the full length nucleic acid sequence (i.e. SEQ ID NO: 1).**

In addition, Stemmer teaches using his method (i.e. recursive DNA shuffling by fragmentation, reassembly and selection) to improve and/or optimize the yield, stability, and/or enzymatic capability of proteins. Therefore, absent an unexpected result it would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention to modify the method of Stemmer wherein a recombinant DNA vector encoding an endoglucanase and comprising a sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto as taught by Knowles et al. was mutagenized. The motivation for making the modification recited above would have been to improve and/or optimize the yield, stability, and/or enzymatic capability of the endoglucanase taught by Knowles et al. Also, absent an unexpected result, the substitution of one well known reagent with known properties for a second well known reagent with known properties is routine in the art. As regards the motivation to make the substitution recited above, the motivation to combine arises from the expectation that the prior art elements will perform their expected functions to achieve

their expected results when combined for their common known purpose. Support for making this obviousness rejection comes from the M.P.E.P. at 2144.07 and 2144.09.

**Claim 97** is drawn to an embodiment of Claim **93** or 95 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 55% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 93 above.

**Claim 98** is drawn to an embodiment of Claim 97 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 60% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 93 above.

**Claim 110** is drawn to an embodiment of the method of Claim **93** or 95 wherein the endoglucanase activity comprises a carboxymethyl cellulase activity.

Admittedly, Knowles et al. do not explicitly teach that their recombinant enzyme(s) (i.e. their endoglucanase(s) comprise a carboxymethyl cellulase activity. However, absent a showing to the contrary, its is believed that this limitation is inherent to the endoglucanase(s) taught by Knowles et al.

**Claim 111** is drawn to a method of generating and identifying a nucleic acid encoding an endoglucanase which comprises three required steps. To begin, a nucleic acid encoding an endoglucanase comprising a sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto is obtained. Next, one or more nucleotides in said sequence are modified to another nucleotide deleting one or more nucleotides in the sequence or adding one or more nucleotides to said sequence. Finally, a modified nucleic acid encoding a polypeptide having an endoglucanase activity is identified.

Stemmer teaches a method of mutagenesis which comprises all of the limitations set forth in Claim 111 except these authors do not teach a nucleic acid as recited in Claim 111. However, Knowles et al. do teach a recombinant DNA vector encoding an endoglucanase (i.e. EGI) and comprising a nucleic acid sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1. **Note that the phrase "comprising a sequence" in Claim 111 has been interpreted broadly to mean two nucl otid s. The phrasing used (i.e. "comprising a sequenc ") can be int rpr ted to mean two nucleotides all the way up to the full length nucleic acid sequence (i.e. SEQ ID NO: 1). Also, not the alignment provided by the applicant and see at least nucleotide positions 2280-2309 of applicant's SEQ ID NO: 1 and not that the sequence of Knowles et al. (i.e. the sequ nce**

**in the top row) comprises a sequence of least 30 consecutive residues which has 18/30 (60%) identical nucleotides (i.e. has at least about 50% sequence identity) to a sequence as set forth in SEQ ID NO: 1".**

In addition, Stemmer teaches using his method (i.e. recursive DNA shuffling by fragmentation, reassembly and selection) to improve and/or optimize the yield, stability, and/or enzymatic capability of proteins. Therefore, absent an unexpected result it would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention to modify the method of Stemmer wherein a recombinant DNA vector encoding an endoglucanase and comprising a sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto as taught by Knowles et al. was mutagenized and then identified. The motivation for making the modification recited above would have been to improve and/or optimize the yield, stability, and/or enzymatic capability of the endoglucanase taught by Knowles et al. Also, absent an unexpected result, the substitution of one well known reagent with known properties for a second well known reagent with known properties is routine in the art. As regards the motivation to make the substitution recited above, the motivation to combine arises from the expectation that the prior art elements will perform their expected functions to achieve their expected results when combined for their common known purpose. Support for making this obviousness rejection comes from the M.P.E.P. at 2144.07 and 2144.09.

**Claim 43** is drawn to an embodiment of the method of Claim 42 wherein the modifications are introduced by a method selected from a defined group which includes error-prone PCR, and shuffling.

Stemmer et al. teaches these limitations. See, at least, for example, Claims 1 and 15-19.

**Claim 44** is drawn to an embodiment of the method of Claim 42 wherein the modifications are introduced by error-prone PCR.

Stemmer et al. teaches this limitation. See, at least, for example, Claims 1 and 15-19.

**Claim 45** is drawn to an embodiment of the method of Claim 42 wherein the modifications are introduced by shuffling.

Stemmer et al. teaches this limitation. See, at least, for example, Claims 1 and 15-19.

**Claim 46** is drawn to an embodiment of the method of Claim 42 wherein the modifications are introduced by oligonucleotide-directed mutagenesis.

Stemmer et al. teaches this limitation. See, at least, for example, Claims 1 and 15-19.

**Claim 47** is drawn to an embodiment of the method of Claim 42 wherein the modifications are introduced by assembly PCR.

Admittedly, Stemmer does not explicitly say assembly PCR, however, this limitation is, absent a showing to the contrary, considered to be inherent to Stemmer because recursive DNA shuffling by fragmentation, reassembly and selection is just that assembly PCR . In addition it has also been called sexual PCR mutagenesis by Stemmer. See Stemmer [US6,518,065 (2003)]. Also see, at least, for example, Claims 1 and 15-19 and Figure 1 of Stemmer [US 6,277,638 (2001)].

**Claim 48** is drawn to an embodiment of the method of Claim 42 wherein the modifications are introduced by sexual PCR mutagenesis.

Admittedly, Stemmer does not explicitly say sexual PCR mutagenesis, however, this limitation is, absent a showing to the contrary, considered to be inherent to Stemmer because recursive DNA shuffling by fragmentation, reassembly and selection is just that sexual PCR mutagenesis which is also called assembly PCR. See, at least, for example, Claims 1 and 15-19 and Figure 1. Note also, Stemmer [US6,518,065 (2003)] wherein this author defines recursive DNA shuffling by fragmentation, reassembly and selection as being sexual PCR mutagenesis.

**Claim 54** is drawn to an embodiment of the method of Claim 42 wherein the modifications are introduced by gene reassembly.

For the reasons cited above against Claim 47, Stemmer et al. teaches this limitation. See, at least, for example, Claims 1 and 15-19.

**Claims 49-53 and 55** are drawn to embodiments of the method of Claim 42 wherein the modifications are introduced by a particular type of mutagenesis, all of which were well known at the time of invention. See Column 2, beginning at about line 38 and see the references cited p.3 and Arkin et al. (PNAS 1992). Please note that, absent an unexpected result, the substitution of one method with well known properties and outcomes for a second well known method with known properties and outcomes is routine in the art. As regards the motivation to make the substitution recited above, the motivation to combine arises from the expectation that the prior art elements will perform their expected functions to achieve their expected results when combined for their common known purpose. Support for making this obviousness rejection comes from the M.P.E.P. at 2144.07 and 2144.09

**10.** **Claim(s) 42-55, 93-94, 97-104 and 110-111** is/are rejected under 35 U.S.C. 103(a) as being unpatentable over Stemmer [US 6,277,638 (2001)] in view of Thomas et al. [US 5,536,655 (1996)].

**Claim 42** is drawn to a method of generating a variant which comprises two required steps. To begin, a nucleic acid encoding an endoglucanase comprising a sequence having at least about 50% sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto is obtained. Next one or more nucleotides in said sequence are modified to another nucleotide or one or more nucleotides in said sequence are deleted or one or more nucleotides are added to said sequence.

Stemmer teaches a method of mutagenesis which comprises all of the limitations set forth in Claim 42 except these authors do not teach a nucleic acid as recited in Claim 42. However, Thomas et al. do teach a recombinant DNA vector encoding an endoglucanase (i.e. EGI) and comprising a nucleic acid sequence having at least about 50% sequence identity to a sequence as set forth in SEQ ID NO: 1. **Note that the phrase "comprising a sequence" in Claim 42 has been interpreted broadly to mean two nucleotides. The phrasing used (i.e. "comprising a sequence") can be interpreted to mean two nucleotides all the way up to the full length nucleic acid sequence (i.e. SEQ ID NO: 1). Also, note the alignment provided by the examiner in attached Appendix A. Note nucleotides 1925-1954 of SEQ ID NO:6 of Thomas et al. as compared to nucleotides 1006-1035 of SEQ ID NO: 1 of the instant application. Note that the sequence of Thomas et al. (i.e. the sequence in the top row) comprises a sequence of least 30 consecutive residues which has 27/30 (90%) identical nucleotid s (i.e. it has at least about 50% sequence identity to a sequence of at least 30 consecutive residues as set forth in SEQ ID NO: 1").**

In addition, Stemmer teaches using his method (i.e. recursive DNA shuffling by fragmentation, reassembly and selection) to improve and/or optimize the yield, stability, and/or enzymatic capability of

proteins. Therefore, absent an unexpected result, it would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention to modify the method of Stemmer et al. wherein a recombinant DNA vector encoding an endoglucanase and comprising a sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto as taught by Thomas et al. was mutagenized. Note that Thomas et al. also teaches mutagenesis. The motivation for making the modification recited above would have been to improve and/or optimize the yield, stability, and/or enzymatic capability of the endoglucanase taught by Thomas et al. Also, absent an unexpected result, the substitution of one well known reagent with well known properties for a second well known /method reagent with known properties is routine in the art. As regards the motivation to make the substitution recited above, the motivation to combine arises from the expectation that the prior art elements will perform their expected functions to achieve their expected results when combined for their common known purpose. Support for making this obviousness rejection comes from the M.P.E.P. at 2144.07 and 2144.09.

**Claim 93** is drawn to a method of generating a nucleic acid encoding an endoglucanase which method comprises two required steps. To begin, a nucleic acid encoding an endoglucanase, wherein the nucleic acid comprises at least 30 consecutive residue of a sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto is obtained. Next one or more nucleotides in said sequence are modified to another nucleotide deleting one or more nucleotides in the sequence or adding one or more nucleotides in the sequence are added to said sequence.

Stemmer teaches a method of mutagenesis which comprises all of the limitations set forth in Claim 93 except these authors do not teach a nucleic acid as recited in Claim 93. However, Thomas et al. do teach a recombinant DNA vector encoding an endoglucanase (i.e. EGI) and "comprising at least 30 consecutive residue of a sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1". **Note the alignment provided by the examiner in attached Appendix A. Note nucleotides 1925-1954 of SEQ ID NO:6 of Thomas et al. as compared to nucleotides 1006-1035 of SEQ ID NO: 1 of the instant application. Note that the sequence of Thomas et al. (i.e. the sequence in the top row) comprises a sequence of least 30 consecutive residues which has 27/30 (90%) identical nucleotides (i.e. it has at least about 50% sequence identity to a sequence of at least 30 consecutive residues as set forth in SEQ ID NO: 1").**

In addition, Stemmer teaches using his method (i.e. recursive DNA shuffling by fragmentation, reassembly and selection) to improve and/or optimize the yield, stability, and/or enzymatic capability of proteins. Therefore, absent an unexpected result it would have been *prima facie* obvious to one of

ordinary skill in the art at the time of the invention to modify the method of Stemmer wherein a recombinant DNA vector encoding an endoglucanase and comprising a sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto as taught by Thomas et al. was mutagenized. Note that Thomas et al. also teaches mutagenesis. The motivation for making the modification recited above would have been to improve and/or optimize the yield, stability, and/or enzymatic capability of the endoglucanase taught by Thomas et al. Also, absent an unexpected result, the substitution of one well known reagent with well known properties for a second well known /method reagent with known properties is routine in the art. As regards the motivation to make the substitution recited above, the motivation to combine arises from the expectation that the prior art elements will perform their expected functions to achieve their expected results when combined for their common known purpose. Support for making this obviousness rejection comes from the M.P.E.P. at 2144.07 and 2144.09.

**Claim 94** is drawn to a method of generating a nucleic acid encoding an endoglucanase which method comprises two required steps. To begin, a nucleic acid comprising a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto is obtained. Next one or more nucleotides in said sequence are modified to another nucleotide, deleting one or more nucleotides in the sequence or adding one or more nucleotides in the sequence are added to said sequence.

Stemmer teaches a method of mutagenesis which comprises all of the limitations set forth in Claim 94 except these authors do not teach a nucleic acid as recited in Claim 94. However, Thomas et al. do teach a recombinant DNA vector encoding an endoglucanase (i.e. EGI) and comprising a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto. **Note that the phrase "comprising a sequence" in Claims 94 has been interpreted broadly to mean two nucleotides. The phrasing used (i.e. "comprising a sequence") can be reasonably interpreted to mean - two nucleotides all the way up to the full length nucleic acid sequence (i.e. SEQ ID NO: 1).**

In addition, Stemmer teaches using his method (i.e. recursive DNA shuffling by fragmentation, reassembly and selection) to improve and/or optimize the yield, stability, and/or enzymatic capability of proteins. Therefore, absent an unexpected result it would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention to modify the method of Stemmer wherein a recombinant DNA vector encoding an endoglucanase and comprising a sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto as taught by Thomas et al. was mutagenized. Note that Thomas et al. also teaches mutagenesis. The motivation for making the modification recited above would have been to improve and/or optimize the

yield, stability, and/or enzymatic capability of the endoglucanase taught by Thomas et al. Also, absent an unexpected result, the substitution of one well known reagent with well known properties for a second well known /method reagent with known properties is routine in the art. As regards the motivation to make the substitution recited above, the motivation to combine arises from the expectation that the prior art elements will perform their expected functions to achieve their expected results when combined for their common known purpose. Support for making this obviousness rejection comes from the M.P.E.P. at 2144.07 and 2144.09.

**Claim 97** is drawn to an embodiment of Claim **93** or 95 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 55% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 93 above.

**Claim 98** is drawn to an embodiment of Claim 97 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 60% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 93 above.

**Claim 99** is drawn to an embodiment of Claim 98 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 65% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 93 above.

**Claim 100** is drawn to an embodiment of Claim 99 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 70% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 93 above.

**Claim 101** is drawn to an embodiment of Claim 100 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 75% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 93 above.

**Claim 102** is drawn to an embodiment of Claim 101 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 80% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 93 above.

**Claim 103** is drawn to an embodiment of Claim 102 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 85% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 93 above.

**Claim 104** is drawn to an embodiment of Claim 103 wherein the nucleic acid comprises at least 30 consecutive residues of a sequence having at least about 90% sequence identity to a sequence as set forth in SEQ ID NO: 1.

See the rejection of Claim 93 above.

**Claim 43** is drawn to an embodiment of the method of Claim 42 wherein the modifications are introduced by a method selected from a defined group which includes error-prone PCR, and shuffling.

Stemmer et al. teaches these limitations. See, at least, for example, Claims 1 and 15-19.

**Claim 44** is drawn to an embodiment of the method of Claim 42 wherein the modifications are introduced by error-prone PCR.

Stemmer et al. teaches this limitation. See, at least, for example, Claims 1 and 15-19.

**Claim 45** is drawn to an embodiment of the method of Claim 42 wherein the modifications are introduced by shuffling.

Stemmer et al. teaches this limitation. See, at least, for example, Claims 1 and 15-19.

**Claim 46** is drawn to an embodiment of the method of Claim 42 wherein the modifications are introduced by oligonucleotide-directed mutagenesis.

Stemmer et al. teaches this limitation. See, at least, for example, Claims 1 and 15-19.

**Claim 47** is drawn to an embodiment of the method of Claim 42 wherein the modifications are introduced by assembly PCR.

Admittedly, Stemmer does not explicitly say assembly PCR, however, this limitation is, absent a showing to the contrary, considered to be inherent to Stemmer because recursive DNA shuffling by fragmentation, reassembly and selection is just that assembly PCR . In addition it has also been called sexual PCR mutagenesis by Stemmer. See Stemmer [US 6,518,065 (2003)]. Also see, at least, for example, Claims 1 and 15-19 and Figure 1 of Stemmer [US 6,277,638 (2001)].

**Claim 48** is drawn to an embodiment of the method of Claim 42 wherein the modifications are introduced by sexual PCR mutagenesis.

Admittedly, Stemmer does not explicitly say sexual PCR mutagenesis, however, this limitation is, absent a showing to the contrary, considered to be inherent to Stemmer because recursive DNA shuffling by fragmentation, reassembly and selection is just that sexual PCR mutagenesis which is also called assembly PCR. See, at least, for example, Claims 1 and 15-19 and Figure 1. Note also, Stemmer [US 6,518,065 (2003)] wherein this author defines recursive DNA shuffling by fragmentation, reassembly and selection as being sexual PCR mutagenesis.

**Claim 54** is drawn to an embodiment of the method of Claim 42 wherein the modifications are introduced by gene reassembly.

For the reasons cited above against Claim 47, Stemmer et al. teaches this limitation. See, at least, for example, Claims 1 and 15-19.

**Claims 49-53 and 55** are drawn to embodiments of the method of Claim 42 wherein the modifications are introduced by a particular type of mutagenesis, all of which were well known at the time of invention. See Column 2, beginning at about line 38 and see the references cited p.3 and Arkin et al. (PNAS 1992) Please note that, absent an unexpected result, the substitution of one method with known properties and outcomes for a second well known method with known properties and outcomes is routine in the art. As regards the motivation to make the substitution recited above, the motivation to combine arises from the expectation that the prior art elements will perform their expected functions to achieve their expected results when combined for their common known purpose. Support for making this obviousness rejection comes from the M.P.E.P. at 2144.07 and 2144.09.

**Claim 110** is drawn to an embodiment of the method of Claim **93** or 95 wherein the endoglucanase activity comprises a carboxymethyl cellulase activity.

Admittedly, Thomas et al. do not explicitly teach that their recombinant enzyme(s) (i.e. their endoglucanase(s) comprise a carboxymethyl cellulase activity. However, absent a showing to the contrary, its is believed that this limitation is inherent to the endoglucanase(s) taught by Thomas et al.

**Claim 111** is drawn to a method of generating and identifying a nucleic acid encoding an endoglucanase which comprises three required steps. To begin, a nucleic acid encoding an endoglucanase comprising a sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto is obtained. Next, one or more nucleotides in said sequence are modified to another nucleotide deleting one or more nucleotides in the sequence or adding one or more nucleotides to said sequence. Finally, a modified nucleic acid encoding a polypeptide having an endoglucanase activity is identified.

Stemmer teaches a method of mutagenesis which comprises all of the limitations set forth in Claim 111 except these authors do not teach a nucleic acid as recited in Claim 111. However, Thomas et al. do teach a recombinant DNA vector encoding an endoglucanase (i.e. EGI) and comprising a nucleic acid sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1. **Note that the phrase "comprising a sequence" in Claim 111 has been interpreted broadly to mean two nucleotides. The phrasing used (i.e. "comprising a sequence") can be interpreted to mean two nucleotides all the way up to the full length nucleic acid sequence (i.e. SEQ ID NO: 1). Also, note the alignment provided by the examiner in attached Appendix A. Note nucleotides 1925-1954 of SEQ ID NO:6 of Thomas et al. as compared to nucleotides 1006-1035 of SEQ ID NO: 1 of the instant application. Note that the sequence of Thomas et al. (i.e. the sequence in the top row) comprises a sequence of least 30 consecutive residues which has 27/30 (90%) identical nucleotides (i.e. it has at least about 50% sequence identity to a sequence of at least 30 consecutive residues as set forth in SEQ ID NO: 1").**

In addition, Stemmer teaches using his method (i.e. recursive DNA shuffling by fragmentation, reassembly and selection) to improve and/or optimize the yield, stability, and/or enzymatic capability of proteins. Also note that Thomas et al. expressly teach mutagenesis to prepare their recombinant proteins with additional enzymatic activities. Therefore, absent an unexpected result it would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention to modify the method of Stemmer wherein a recombinant DNA vector encoding an endoglucanase and comprising a sequence having at least about 50 % sequence identity to a sequence as set forth in SEQ ID NO: 1 or sequences complementary thereto as taught by Thomas et al. was mutagenized and then identified. The motivation for making the modification recited above would have been to improve and/or optimize the yield, stability, and/or enzymatic capability of the endoglucanase taught by Thomas et al. Also, absent an unexpected result, the substitution of one well known reagent with known properties for a second well known reagent with known properties is routine in the art. As regards the motivation to make the substitution recited above, the motivation to combine arises from the expectation that the prior art elements will perform their expected functions to achieve their expected results when combined for their

common known purpose. Support for making this obviousness rejection comes from the M.P.E.P. at 2144.07 and 2144.09.

## CLAIM OBJECTIONS

**11.** **Claim(s) 105-109** is /are objected to because it/they is/are dependent upon a rejected independent base claim.

## RESPONSE TO APPLICANT'S AMENDMENT/ ARGUMENTS

**12.** Applicant's arguments with respect to the claimed invention have been fully and carefully considered but are moot in view of the new ground(s) of rejection.

## CONCLUSION

**1.** **Claim(s) 42-55 and 88-112** is/are rejected and/or objected to for the reason(s) set forth above.

**2.** Applicant's amendment necessitated the new grounds of rejection. Accordingly, **THIS ACTION IS MADE FINAL.** See M.P.E.P. § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 C.F.R. § 1.136(a).

A SHORTENED STATUTORY PERIOD FOR RESPONSE TO THIS FINAL ACTION IS SET TO EXPIRE THREE MONTHS FROM THE DATE OF THIS ACTION. IN THE EVENT A FIRST RESPONSE IS FILED WITHIN TWO MONTHS OF THE MAILING DATE OF THIS FINAL ACTION AND THE ADVISORY ACTION IS NOT MAILED UNTIL AFTER THE END OF THE THREE-MONTH SHORTENED STATUTORY PERIOD, THEN THE SHORTENED STATUTORY PERIOD WILL EXPIRE ON THE DATE THE ADVISORY ACTION IS MAILED, AND ANY EXTENSION FEE PURSUANT TO 37 C.F.R. § 1.136(a) WILL BE CALCULATED FROM THE MAILING DATE OF THE ADVISORY ACTION. IN NO EVENT WILL THE STATUTORY PERIOD FOR RESPONSE EXPIRE LATER THAN SIX MONTHS FROM THE DATE OF THIS FINAL ACTION.

**3.** Any inquiry concerning this communication or earlier communications from the examiner should be directed to Ethan Whisenant, Ph.D. whose telephone number is (703) 308-6567. The examiner can normally be reached Monday-Friday from 8:30AM -5:30PM EST or any time via voice mail. If repeated

attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, W. Gary Jones, can be reached at (703) 308-1152.

The fax number for this Examiner is (703) 746-8465. Before faxing any papers please inform the examiner to avoid lost papers. Please note that the faxing of papers must conform with the Notice to Comply published in the Official Gazette, 1096 OG 30 (November 15, 1989). Any inquiry of a general nature or relating to the status of this application should be directed to the group receptionist whose telephone number is (703) 308-0196.

ETHAN WHISENANT
PRIMARY EXAMINER

# Appendix A